Supplementary Materials

Supplementary Material, Figure 1

Correlation analysis generated in Rosetta Resolver software. For each vehicle vs E_2 data were plotted against vehicle vs xenoestrogen. Correlation coefficients of common signature genes were compared to give an indication of how similar the responses were.

Supplementary Material, Figure 2

Comparison of uterine gene response profiles after 2 hours (A) or 24 hours (B). Hierarchical clusters were built in Rosetta Resolver using cutoffs of $p<0.001$ and at least 2 fold change in expression of WT or KIKO E_2 BPA or HPTE treatment. Each horizontal row represents comparison of vehicle to an estrogenic substance (E_2, BPA or HPTE) for the indicated ERα genotype (WT, KIKO or αERKO). Genes increased relative to vehicle treated are red; decreased are green.

Supplementary Material, Figure 3

Correlation analysis generated in Rosetta Resolver software. For each KIKO vehicle vs E_2 data were plotted against KIKO vehicle vs xenoestrogen. Correlation coefficients of common signature genes were compared to give an indication of how similar the responses were.

Supplementary Material, Figure 4

Correlation analysis generated in Rosetta Resolver software. KIKO vehicle vs E_2 data were plotted against WT vehicle vs E_2. Correlation coefficients of common signature genes were compared to give an indication of how similar the responses were.

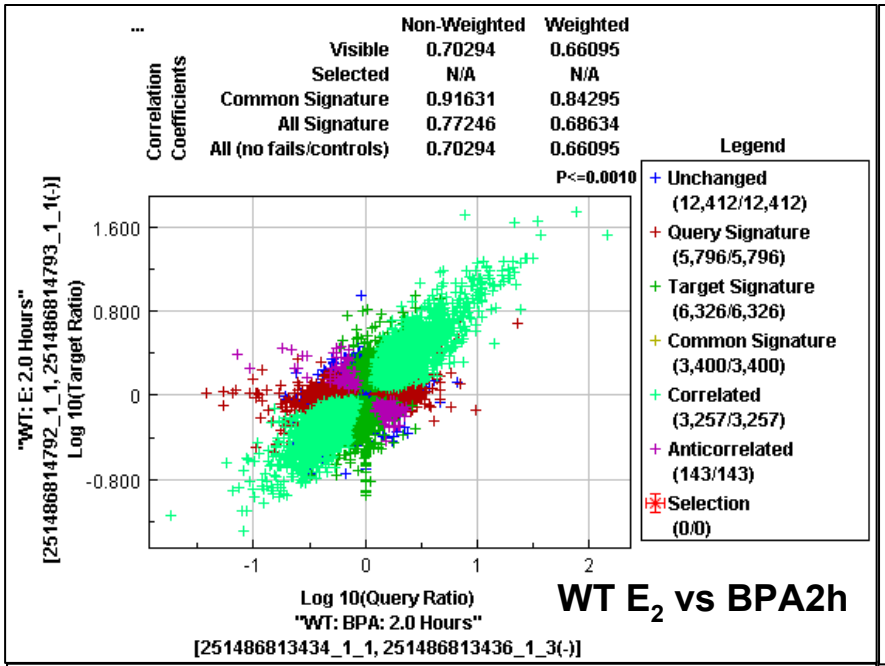
Supplementary Material, Figure 5

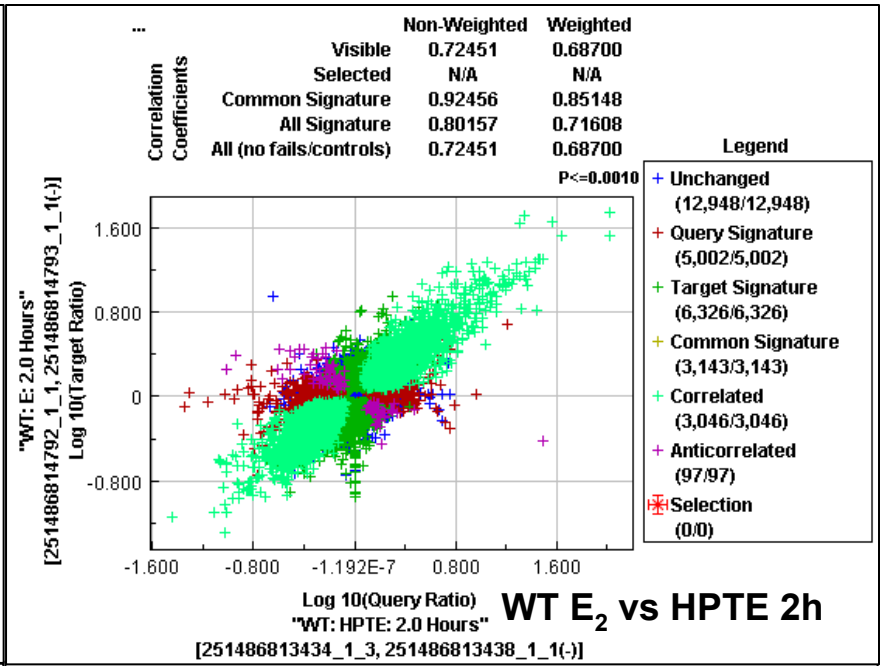
RT-PCR analysis of WT and Ex3αERKO samples for transcripts that have residual responses in the αERKO. Note that unlike the results in Figure 3A in this experiment, the xenoestrogen responses in the WT were as robust as E_2. Results were analyzed by 2 way ANOVA with a post t test relative to V. **: $P<0.01$

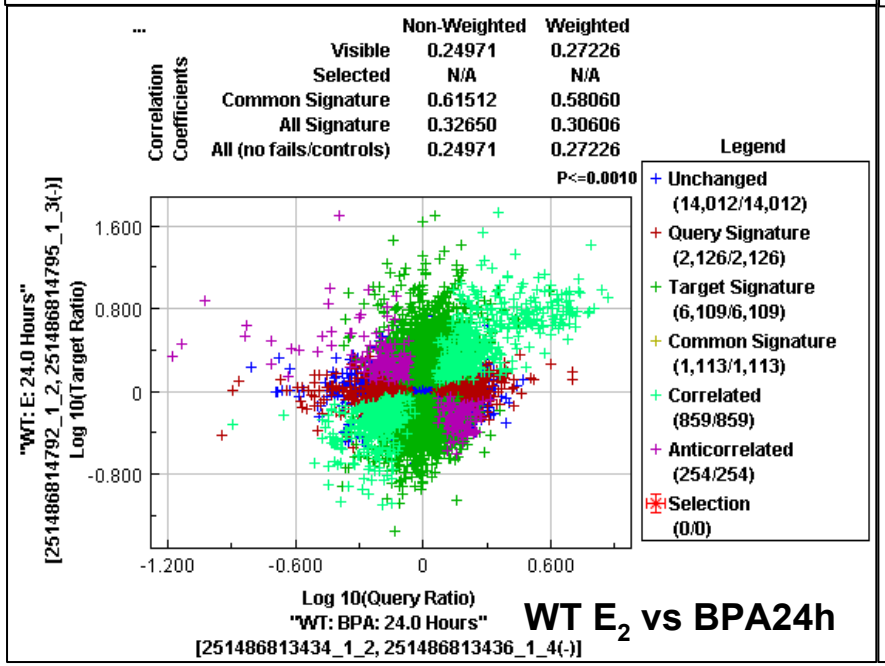
Supplementary Material, Figure 6

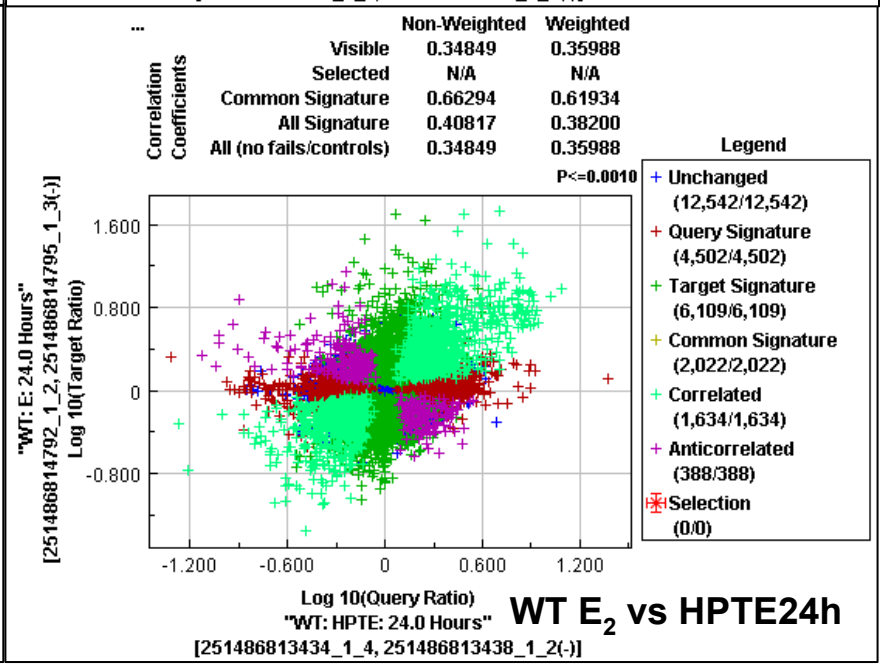
Analysis of potential xenoestrogen selective transcripts

RT-PCR and microarray values of 5 potential xenoestrogen selective transcripts. *Axin1, period homolog 1 (Drosophila) (Per1*), *tenascin XB (Tnxb), guanine nucleotide binding protein, alpha 12 (Gna12),* and *major vault protein (Mvp).* Results were analyzed by 2 way ANOVA relative to V with a post t test. * $P<0.05$



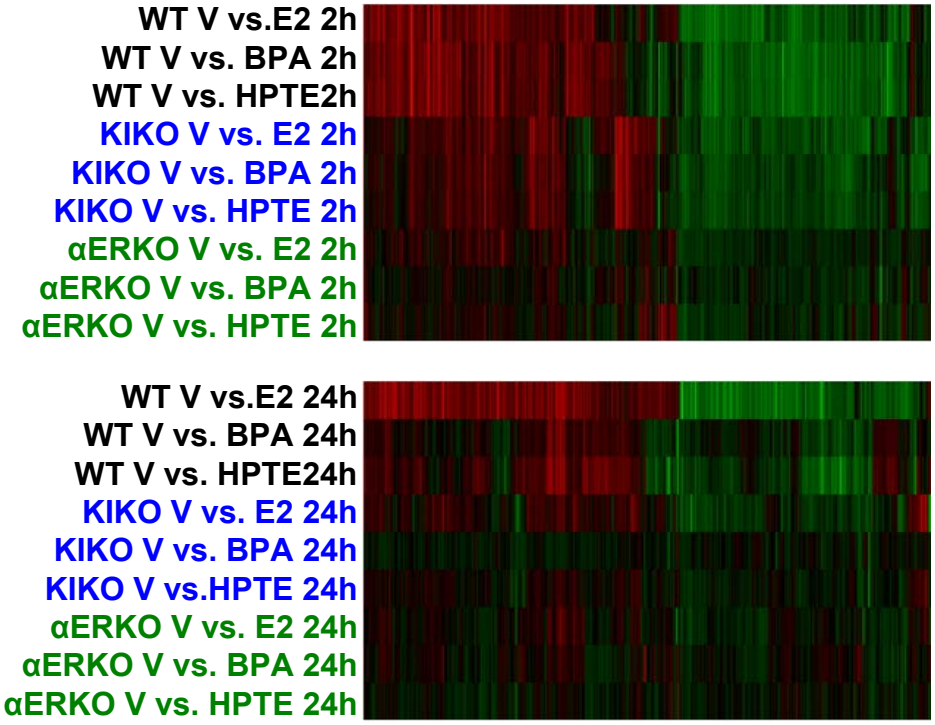






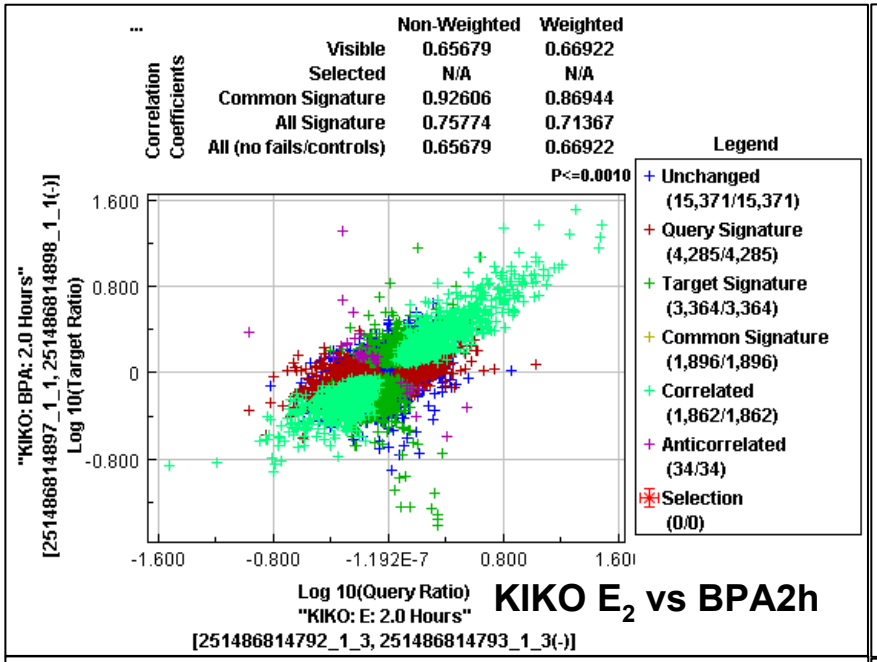
Supplemental Material, Figure 1

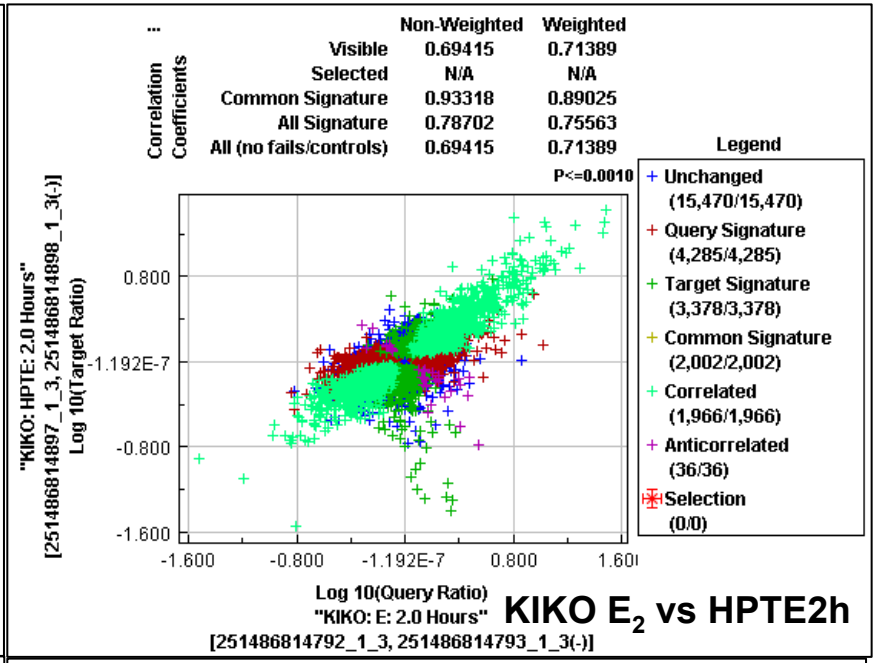
A.

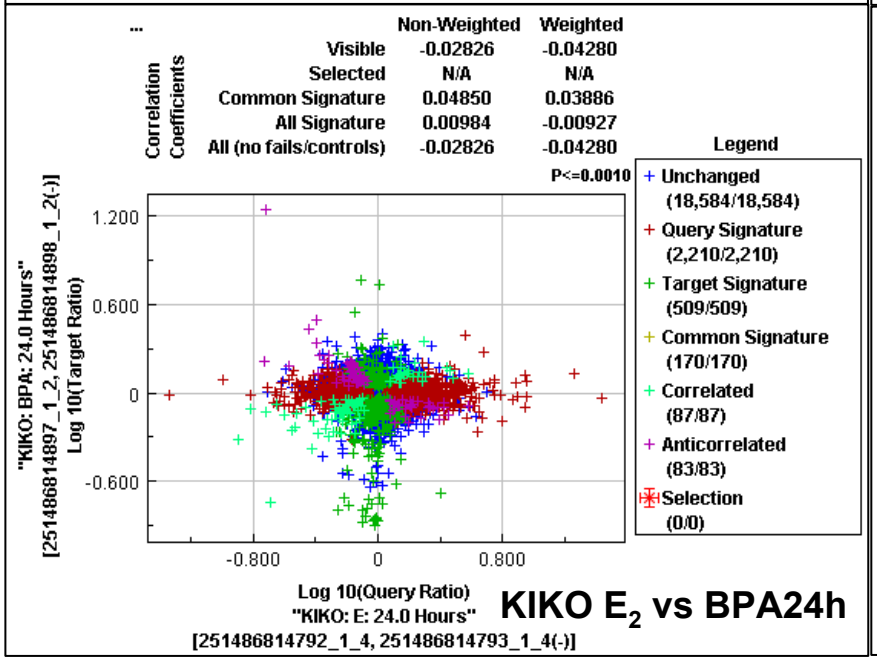


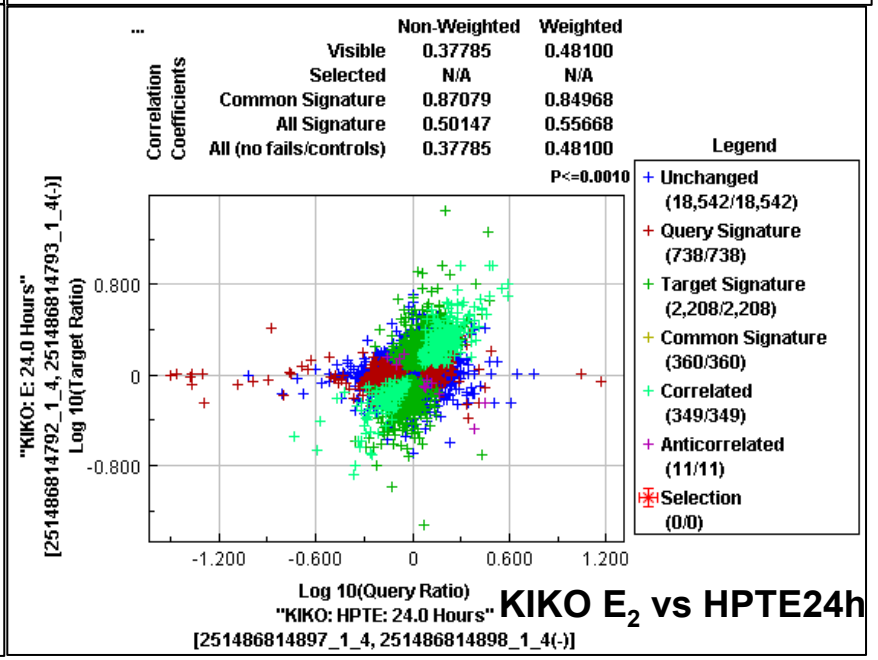
B.

Supplemental Material, Figure 2

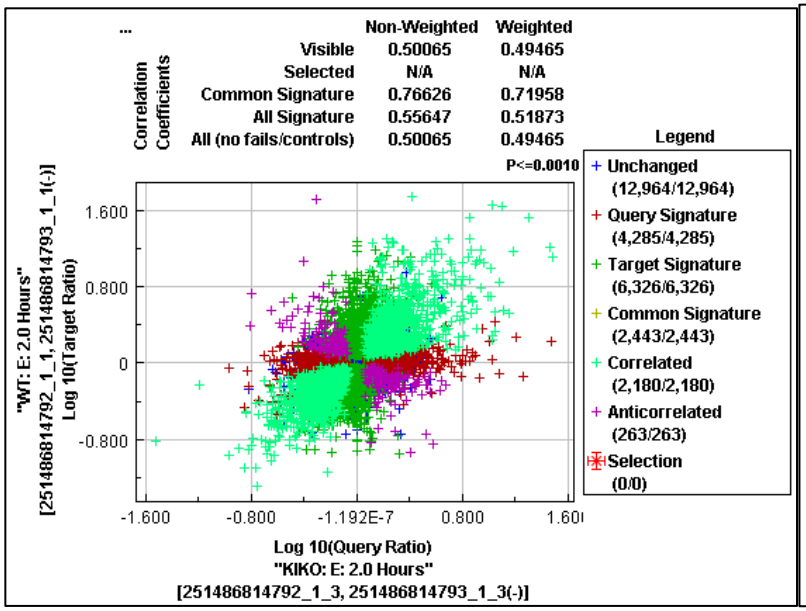




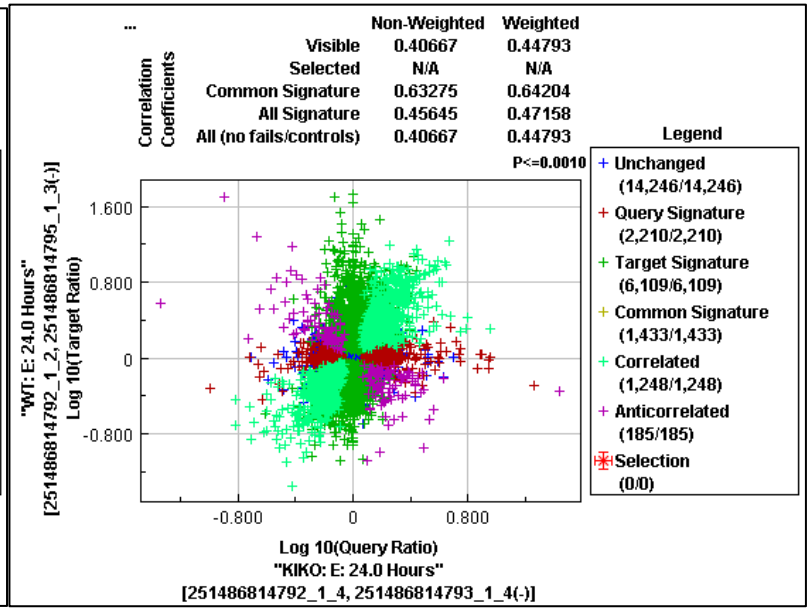




Supplemental Material, Figure 3

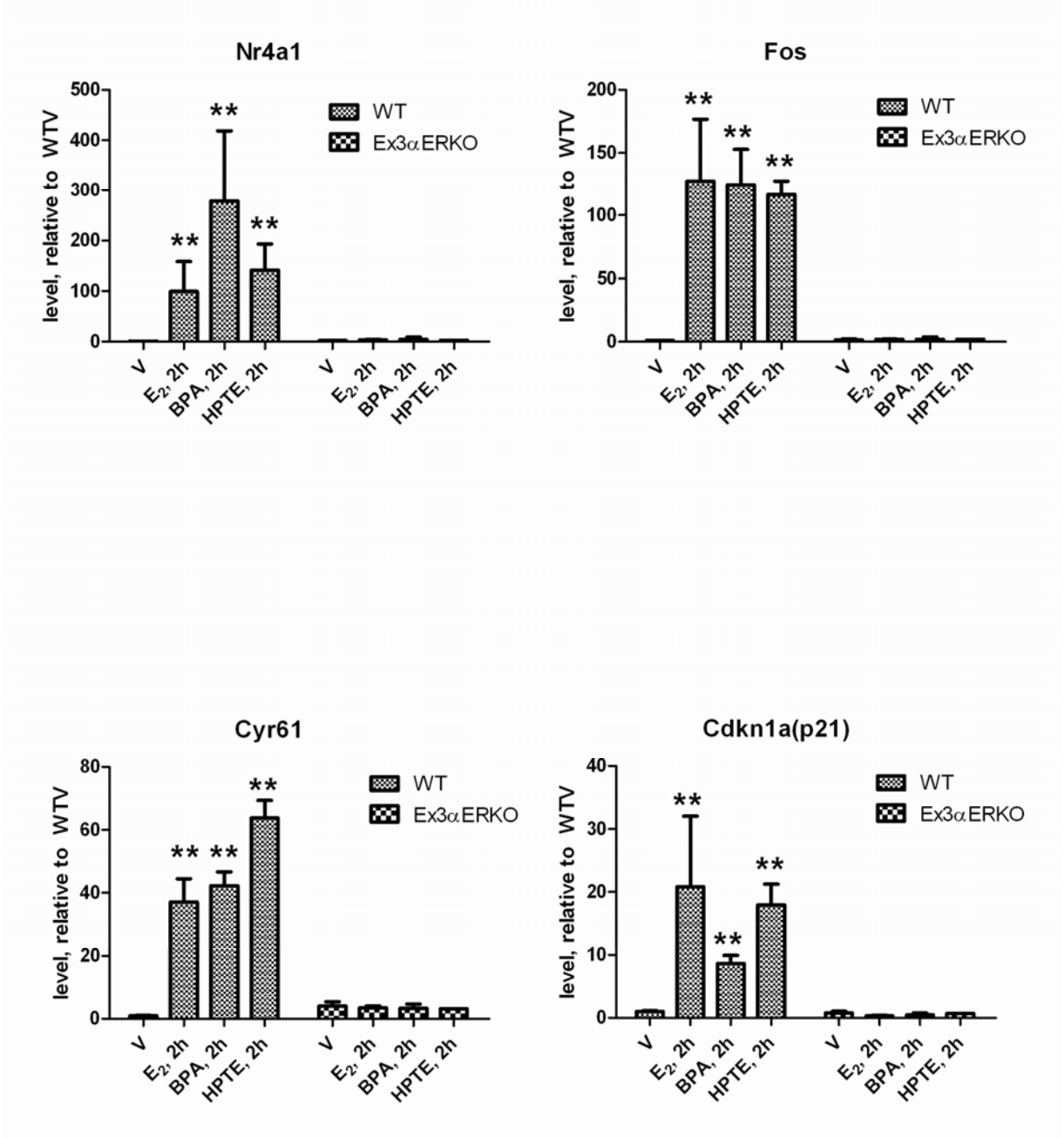


WT vs KIKO E_2 2h



WT vs KIKO E_2 24h

Supplemental Material, Figure 4



Supplemental Material, Figure 5

	E_2, 2h	BPA, 2h	HPTE, 2h
Axin1	**1.14649**	**2.48124**	**2.15126**
Per1	**1.12269**	**3.98242**	**2.7471**
Tnxb	**-1.06701**	**2.4531**	**2.24406**
Gna12	**-1.1475**	**2.0695**	**1.91834**
Mvp	**-1.35848**	**2.88604**	**2.43668**

Microarray Values
(fold change vs V)

Supplemental Material, Figure